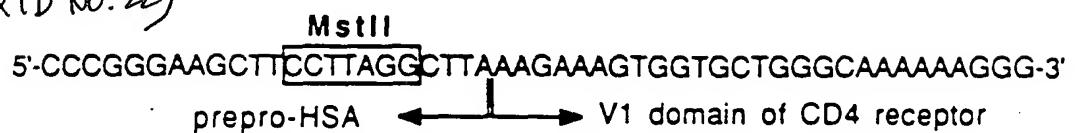


PL I

OLIGODEOXYNUCLEOTIDE Xol26

(SEQ ID NO: 22)



OLIGODEOXYNUCLEOTIDE Xol27

(SEQ ID NO. 23)

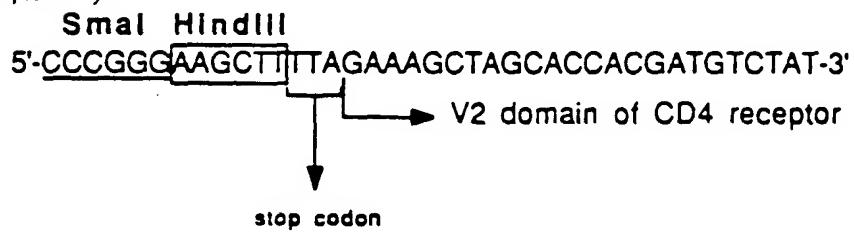


Figure 1

(SEQ ID NO. 24)

MstII

01 11 21 31 41 51 61 71
CCCTAGGCTTAAAGAAAGTGGTGTGGCAAAAAGGGATACTGGAACTGACCTGTACAGCTCCAGAAGA
 76 86 96 106 116 126 136 146
 AGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAAGATTCTGGAAATCAGGGCTCCCTTAACAAAG
 151 161 171 181 191 201 211 221
 GTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTGGGACCAAGGAAACTCCCCCTGATCATCA
 226 236 246 256 266 276 286 296
 AGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGGTGCATTGCTAG
 301 311 321 331 341 351 361 371
 TGTTGGATTGACTGCCAACTCTGACACCCACCTGCTCAGGGGAGAGCCTGACCCCTGACCTGGAGAGCCCCC
 376 386 396 406 416 426 436 446
 CTGGTAGTAGCCCCCTCAGTCAAATGTAGGAGTCCAAGGGTAAAAACATACAGGGGGGAGACCCCTCTCCGTGT
 451 461 471 481 491 501 511 521
 CTCAGCTGGAGCTCCAGGATACTGGCACCTGGACATGCACTGTCTGCAGAACCAAGAAGGAGGTGGAGTTCAAAA
 526 536 546 556
HindIII SmaI
 TAGACATCGTGGTGCTAGCTTCTAAAGCTTCCCCGGG

Figure 2

(SEQ ID No. 26)
(SEQ ID No. 25)

MetLysTrpValThrPheIleSerLeuLeuPheLeuPheSerSerAlaTyrSerArgGlyValPheArg
AAGCTTATGAAAGTGGGTAACCTTATTCCCTCTTCTCTAGCTCGGCTTATTCCAGGGCTGTGTTCTG
1 11 21 31 41 51 61 71

ArgAspAlaHisLysSerGluValAlaHisArgPheLysAspLeuGlyGluGluAsnPheLysAlaLeuValLeu
CGAGATGCACACAGAGTGAGGTTGCTCATCGGTTAAAGATTTGGAGAAGAAAATTCAAAGCCTGGTGTG
76 86 96 106 116 126 136 146

IleAlaPheAlaGlnTyrLeuGlnGlnCysProPheGluAspHisValLysLeuValAsnGluValThrGluPhe
ATTGCCTTGCTCAGTATCTCAGCAGTGTCCATTGAAGATCATGTAAAATTAGTGAATGAAGTAAGTGAATT
151 161 171 181 191 201 211 221

AlaLysThrCysValAlaAspGluSerAlaGluAsnCysAspLysSerLeuHisThrLeuPheGlyAspLysLeu
GCAAAACATGTGGCTGATGAGTCAGCTGAAAATTGTGACAAATCACTTCATACCCCTTTGGAGACAAATT
226 236 246 256 266 276 286 296

CysThrValAlaThrLeuArgGluThrTyrGlyGluMetAlaAspCysCysAlaLysGlnGluProGluArgAsn
TGCACAGTTGCAACTCTTCGTGAAACCTATGGTGAATGGCTGACTGCTGTGCAAAACAAGAACCTGAGAGAAA
301 311 321 331 341 351 361 371

GluCysPheLeuGlnHisLysAspAspAsnProAsnLeuProArgLeuValArgProGluValAspValMetCys
GAATGCTTCTTGCAACACAAAGATGACAACCCAAACCTCCCCGATTGGTGAGACCAGAGGTTGATGTGATGTG
376 386 396 406 416 426 436 446

ThrAlaPheHisAspAsnGluGluThrPheLeuLysLysTyrLeuTyrGluIleAlaArgArgHisProTyrPhe
ACTGCTTTCATGACAATGAAGAGACATTGGAAAAAAACTTATATGAAATTGCCAGAACATCCTTACTTT
451 461 471 481 491 501 511 521

TyrAlaProGluLeuLeuPhePheAlaLysArgTyrLysAlaAlaPheThrGluCysCysGlnAlaAlaAspLys
TATGCCCGGAACTCCTTCTTGCTAAAGGTATAAGCTGCTTTACAGAAIGTGTGCAAGCTGCTGATAAAA
526 536 546 556 566 576 586 596

AlaAlaCysLeuLeuProLysLeuAspGluLeuArgAspGluGlyLysAlaSerSerAlaLysGlnArgLeuLys
GCTGCCTGCCTGTTGCCAAAGCTCGATGAACITCGGGATGAAGGGAAAGGCTCGTCTGCCAACAGAGACTCAAG
601 611 621 631 641 651 661 671

CysAlaSerLeuGlnLysPheGlyGluArgAlaPheLysAlaTrpAlaValAlaArgLeuSerGlnArgPhePro
TGTGCCAGTCTCCAAAATTGGAGAAAGAGCTTCAAAGCATGGCAGTAGCTCGCCTGAGCCAGAGATTCCC
676 686 696 706 716 726 736 746

LysAlaGluPheAlaGluValSerLysLeuValThrAspLeuThrLysValHisThrGluCysCysHisGlyAsp
AAAGCTGAGTTGCAGAACGTTCAAGTTAGTGACAGATCTTACCAAAGCTCACCGGAATGCTGCCATGGAGAT
751 761 771 781 791 801 811 821

LeuLeuGluCysAlaAspAspArgAlaAspLeuAlaLysTyrIleCysGluAsnGlnAspSerIleSerSerLys
CTGCTTGAAATGTGCTGATGACAGGGCGGACCTTGCCAAGTATATCTGTGAAAATCAAGATTGATCTCCAGTAAA
826 836 846 856 866 876 886 896

LeuLysGluCysCysGluLysProLeuLeuGluLysSerHisCysIleAlaGluValGluAsnAspGluMetPro
CTGAAGGAATGCTGTGAAAAACCTCTGTTGGAAAATCCCCTGCAATTGCCGAAGTGGAAAATGATGAGATGCCT
901 911 921 931 941 951 961 971

AlaAspLeuProSerLeuAlaAlaAspPheValGluSerLysAspValCysLysAsnTyrAlaGluAlaLysAsp
GCTGACTTGCCTTCATTAGCTGATTGAAAGTAAGGATGTTGCCAAAAACTATGCTGAGGCCAAAGGAT
976 986 996 1006 1016 1026 1036 1046

Figure 8A

ValPheLeuGlyMetPheLeuTyrGluTyrAlaArgArgHisProAspTyrSerValValLeuLeuLeuArgLeu
 1051 1061 1071 1081 1091 1101 1111 1121
 GTCTTCCTGGGCATGTTTGTATGAATATGCAAGAAGGCATCTGATTACTCTGTCGTACTGCTGAGACTT

 AlaLysThrTyrGluThrThrLeuGluLysCysCysAlaAlaAlaAspProHisGluCysTyrAlaLysValPhe
 1126 1136 1146 1156 1166 1176 1186 1196
 GCCAGACATATGAAACCACTCTAGAGAAGTGTGCGCTGCAGATCCTCATGAATGCTATGCCAAAGTGTTC

 AspGluPheLysProLeuValGluGluProGlnAsnLeuIleLysGlnAsnCysGluLeuPheGluGlnLeuGly
 1201 1211 1221 1231 1241 1251 1261 1271
 GATGAATTTAACCTCTTGTGAAAGAGCCTCAGAATTAAACAAACAAATTGTGAGCTTTGAGCAGCTTGG

 GluTyrLysPheGlnAsnAlaLeuLeuValArgTyrThrLysValProGlnValSerThrProThrLeuVal
 1276 1286 1296 1306 1316 1326 1336 1346
 GAGTACAAATTCCAGAATGCGCTATTAGTTCGTTACACCAAGAAAGTACCCCAAGTGTCAACTCCAACTCTGTA

 GluValSerArgAsnLeuGlyLysValGlySerLysCysCysLysHisProGluAlaLysArgMetProCysAla
 1351 1361 1371 1381 1391 1401 1411 1421
 GAGGTCTCAAGAAACCTAGGAAAGTGGGCAGCAAATGTTGTAAACATCCTGAAGCAAAAGAATGCCCTGTGCA

 GluAspTyrLeuSerValValLeuAsnGlnLeuCysValLeuHisGluLysThrProValSerAspArgValThr
 1426 1436 1446 1456 1466 1476 1486 1496
 GAAGACTATCTATCCGTGGTCTGAAACCAGTTATGTGTGTTGCATGAGAAACGCCAGTAAGTGACAGAGTCACC

 LysCysCysThrGluSerLeuValAsnArgArgProCysPheSerAlaLeuGluValAspGluThrTyrValPro
 1501 1511 1521 1531 1541 1551 1561 1571
 AAATGCTGCACAGAATCCTGGTGAACAGGGCACCATGCTTCTGAAAGTCGATGAAACATACGTTCCC

 LysGluPheAsnAlaGluThrPheThrPheHisAlaAspIleCysThrLeuSerGluLysGluArgGlnIleLys
 1576 1586 1596 1606 1616 1626 1636 1646
 AAAGAGTTAACATGCTGAAACATTCCACCTCCATGCAGATATATGCACACTTCTGAGAAGGAGAGACAAATCAAG

 LysGlnThrAlaLeuValGluLeuValLysHisLysProLysAlaThrLysGluGlnLeuLysAlaValMetAsp
 1651 1661 1671 1681 1691 1701 1711 1721
 AAACAAACTGCACTTGTGAGCTTGTGAAACACAAGCCAAAGCAACAAAGAGCAACTGAAAGCTGTTATGGAT

 AspPheAlaAlaPheValGluLysCysCysLysAlaAspAspLysGluThrCysPheAlaGluGluGlyLysLys
 1726 1736 1746 1756 1766 1776 1786 1796
 GATTCGCAGCTTTGTAGAGAAGTGTGCAAGGCTGACGATAAGGAGACCTGCTTGGCAGGGAGGGTAAAAAAA

 LeuValAlaAlaSerGlnAlaAlaLeuGlyLeuLysLysValValLeuGlyLysLysGlyAspThrValGluLeu
 1801 1811 1821 1831 1841 1851 1861 1871
 CTTGTTGCTGCAAGCTGCTTAAAGAAAGTGGCTGGCAAAAAAGGGATACAGTGGAACTG

 ThrCysThrAlaSerGlnLysLysSerIleGlnPheHisTrpLysAsnSerAsnGlnIleLysIleLeuGlyAsn
 1876 1886 1896 1906 1916 1926 1936 1946
 ACCTGTACAGCTTCCCAGAAGAAGAGCATAACAATTCCACTGGAAAAACTCCAACCAGATAAAGATTCTGGAAAT

 GlnGlySerPheLeuThrLysGlyProSerLysLeuAsnAspArgAlaAspSerArgArgSerLeuTrpAspGln
 1951 1961 1971 1981 1991 2001 2011 2021
 CAGGGCTCCTCTTAACCAAAGGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTGGGACCAA

 GlyAsnPheProLeuIleIleLysAsnLeuLysIleGluAspSerAspThrTyrIleCysGluValGluAspGln
 2026 2036 2046 2056 2066 2076 2086 2096
 GGAAACTTCCCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAAG

 LysGluGluValGlnLeuLeuValPheGlyLeuThrAlaAsnSerAspThrHisLeuLeuGlnGlnSerLeu
 2101 2111 2121 2131 2141 2151 2161 2171
 AAGGAGGAGGTGCAATTGCTAGTGTGCGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGCAGAGCCTG

Figure 8B

ThrLeuThrLeuGluSerProProGlySerSerProSerValGlnCysArgSerProArgGlyLysAsnIleGln
2176 2186 2196 2206 2216 2226 2236 2246
ACCTGACCTTGGAGAGCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGTAAAAACATACAG

GlyGlyLysThrLeuSerValSerGlnLeuGluLeuGlnAspSerGlyThrTrpThrCysThrValLeuGlnAsn
2251 2261 2271 2281 2291 2301 2311 2321
GGGGGGAAAGACCCCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACGTGCTTGCAGAAC

GlnLysLysValGluPheLysIleAspIleValValLeuAlaPhe***
2326 2336 2346 2356 2366 2376
CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTAGCTTCTAAAGCTT

Figure 8C

(SEQ ID No. 28)
(SEQ ID No. 27)

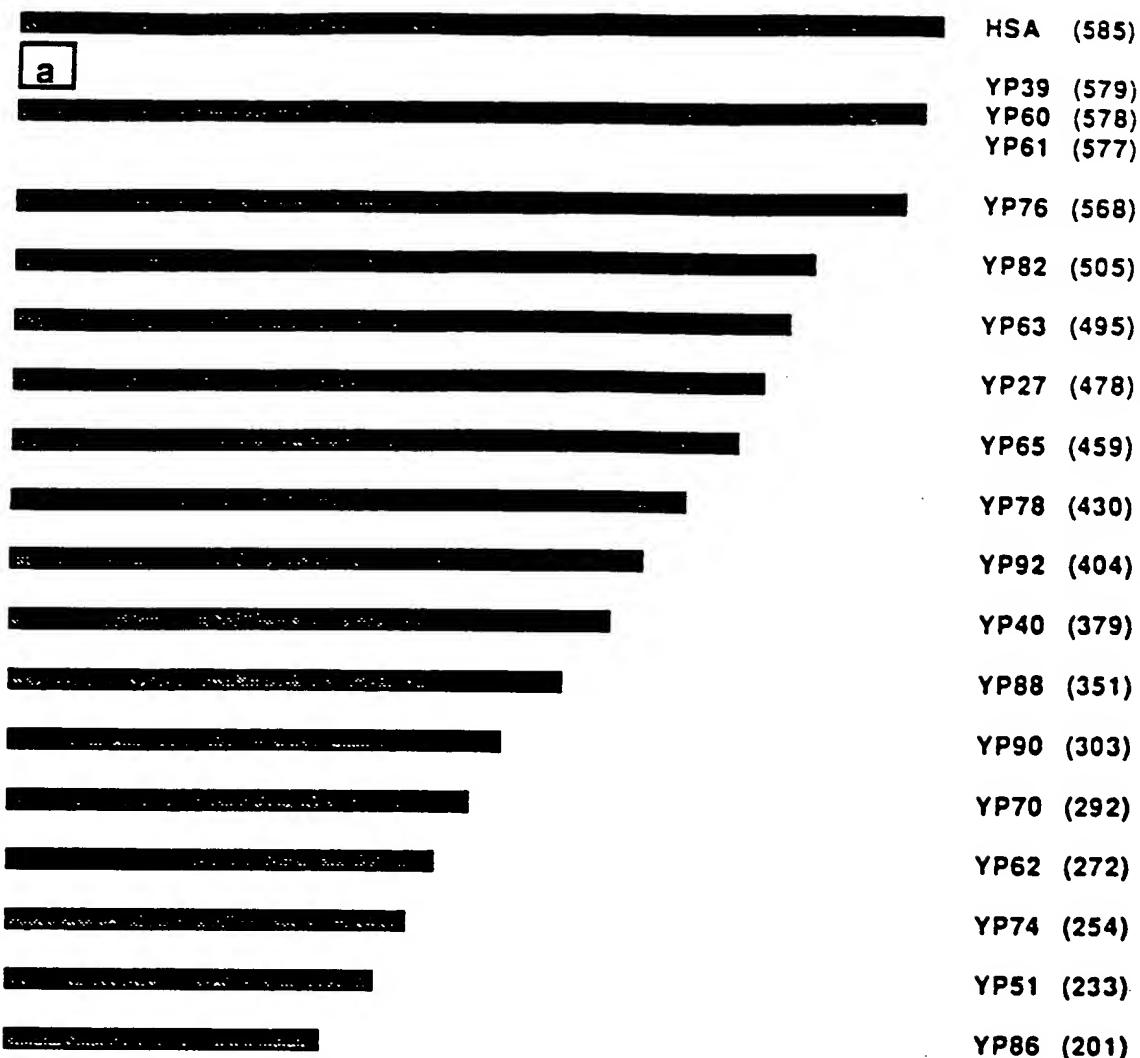
R S L E R I A R L E E K V K T
5' AGATCTTTGGAAAGAATTGCCGTCTGGAAGAAAAAGTGAAGAACT
BgIII

(L) K A Q N S E (L) A S T A N M (L)
CTGAAAGCCCAGAACTCTGAGCTCGCATCCACGCCAACATGCTG

R E Q V A Q (L) K Q L V G D A
CGTGAACACGGTTGCACAGCTGAAGCAACTGGTGGCGACGCC 3'
AhaII



Figure 34



(SEQ ID NO. 30)

b Cys Phe Ser Ala Leu Glu Val Asp [Glu] Thr Tyr Val =====

5' TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT ===== 3'
 (SEQ ID NO. 29)

BAL31 DELETION (YP63)

(SEQ ID NO. 32)

Cys Phe Ser Ala Leu Glu Val Asp Ala Leu Gly =====

5' ===== TCA GCT CTG GAA GTC GAT [GCC TTA GCx] ===== 3'

(SEQ ID NO. 31)

HSA ← MstI

Figure 36

1 (SEQ ID No. 33)

C F A E E G **KK** L V A A S Q A A L G L **KK** V V L G **KK** G D T V E L T C
HSA ← → CD4

2 (SEQ ID No. 34)

S
P
C ----- T L G L K **X** V V L G K **X** G D T V E L T C
HSA ← A → CD4

3 (SEQ ID No. 35)

C F A E E G **K** E D A K G K S E E E A L G L **KK** V V L G **KK** G D T
HSA ← → CD4

4

JUNCTION
PEPTIDE
(OPTIONAL)
C ----- C
HSA ← → CD4

Figure 37

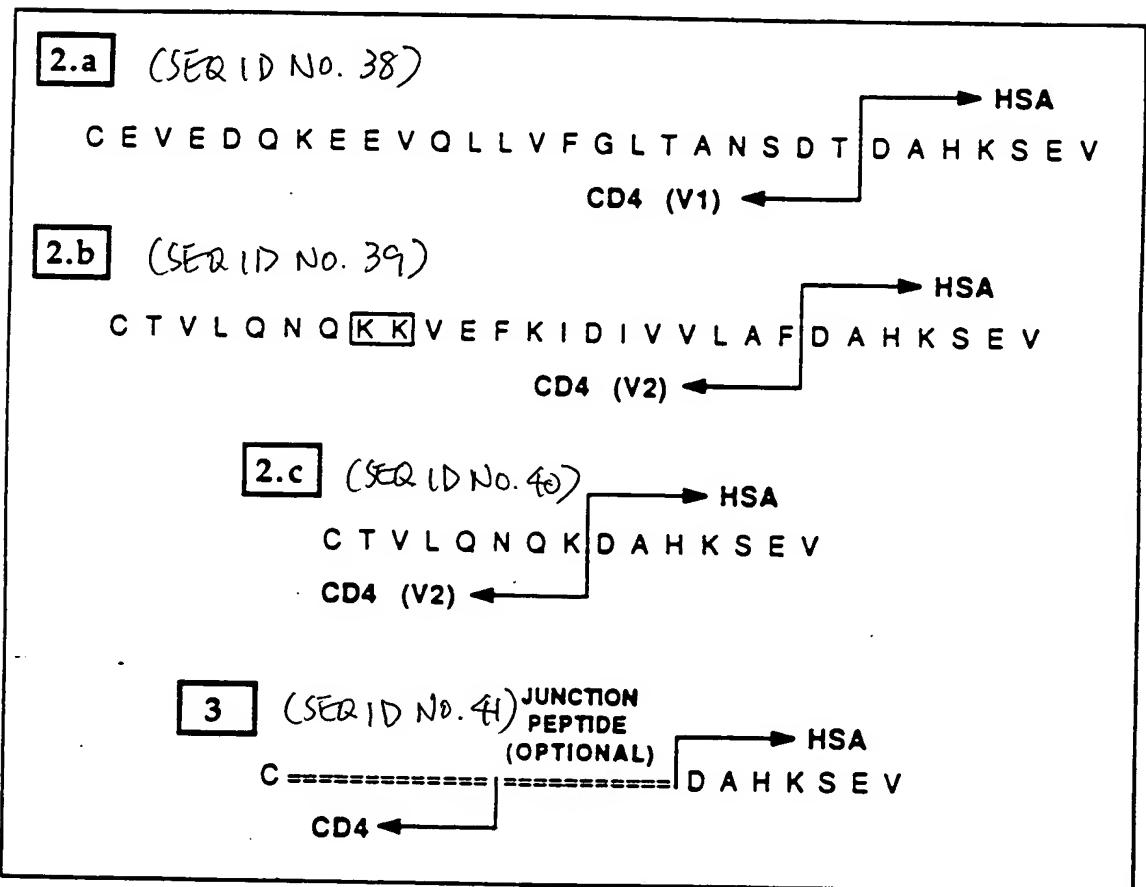
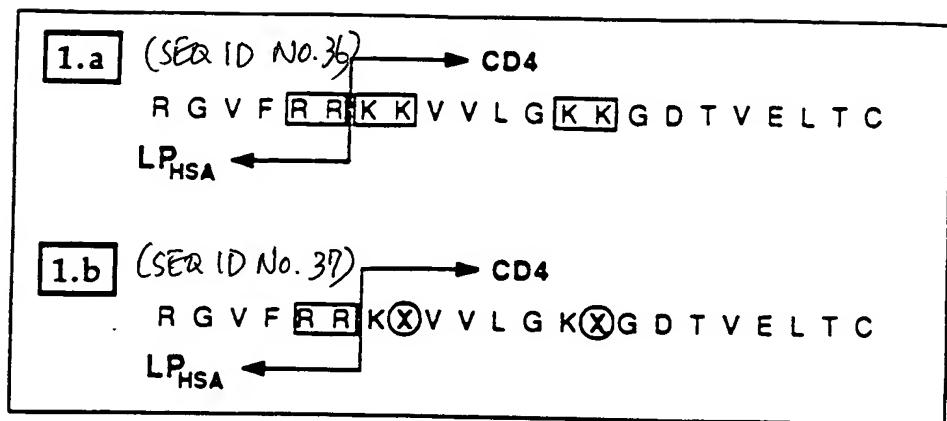


Figure 38